

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 17:18:57 ; Search time 700.96 seconds
(without alignments)
4996.727 Million cell updates/sec

Title: US-09-645-593-8_COPY_1_2040

Perfect score: 2040

Sequence: 1 ctcaagcatcagcagcaggg.....caaaagatcaccacatgsc 2040

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2040	100.0	4999	22	AD03030
2	61	3.0	3501	22	AD03028
3	51.8	2.5	15548	24	ABL34155
C 4	51.2	2.5	17421	22	AAS45349
C 5	51	2.5	40862	24	ABL34073
6	48.6	2.4	1431	21	AZ37082
7	48.6	2.4	1671	13	AAQ24334
C 8	48.2	2.4	5883	24	ABL33732
C 9	48.2	2.4	13326	24	ABL33712

C 10	48	2.4	15548	24	ABL34154	Human immune syste
C 11	48	2.4	18585	24	ABL34609	Human metastasis a
C 12	47.4	2.3	13202	24	ABL33485	Human immune syste
C 13	47.4	2.3	16545	24	ABL32050	Human immune syste
14	47.2	2.3	532	13	AAQ24835	Peroxidase isozyme
15	47.2	2.3	532	21	AAZ98840	Horseradish peroxi
C 16	47.2	2.3	1911	24	ABL34257	Human immune syste
C 17	47.2	2.3	5987	24	ABL33563	Human immune syste
C 18	47.2	2.3	15416	24	ABL34231	Human immune syste
C 19	47.2	2.3	15416	24	AAS61453	Human gene regulat
20	47	2.3	3231	24	ABL34288	Human immune syste
21	46.8	2.3	7498	24	ABL32257	Human immune syste
C 22	46.6	2.3	1500	20	AAZ99536	Nucleic acid sequ
C 23	46.6	2.3	3991	22	AAU16633	Human novel protei
C 24	46.4	2.3	7346	24	ABL32345	Human immune syste
C 25	46.4	2.3	7746	24	ABL33856	Human immune syste
C 26	46.4	2.3	16287	24	ABL32673	Human immune syste
27	45.8	2.2	5962	24	ABL33469	Human immune syste
C 28	45.6	2.2	7498	24	ABL32257	Human immune syste
C 29	45.6	2.2	8991	24	AAS61295	Human gene regulat
C 30	45.4	2.2	1431	21	AAZ37079	DNA sequence encod
C 31	45.4	2.2	14649	22	AAS45414	Chemically pretrea
C 32	45.2	2.2	5378	24	ABL33878	Human immune syste
C 33	44.8	2.2	5430	22	AAS46292	Tumour suppressor
C 34	44.6	2.2	6249	24	ABL33215	Human immune syste
C 35	44.6	2.2	6317	24	ABL32408	Human immune syste
C 36	44.6	2.2	6685	24	ABL32907	Human immune syste
C 37	44.6	2.2	8873	24	AAS61125	Human gene regulat
C 38	44.6	2.2	15416	24	ABL34230	Human immune syste
C 39	44.6	2.2	26997	22	AAS61452	Human gene regulat
40	44.4	2.2	26997	22	AAS46748	Tumour suppressor
41	44.2	2.2	9510	22	AAS46438	Tumour suppressor
42	44.2	2.2	9510	24	ABL34563	Human metastasis a
C 43	44.2	2.2	10326	24	ABL34167	Human immune syste
C 44	44	2.2	12601	22	ABL34206	Human immune syste
C 45	44	2.2	38342	22	AAS46746	Tumour suppressor

ALIGNMENTS

RESULT 1	
AD03030	
ID	AD03030 standard; DNA; 4999 BP.
XX	AC AAD03030;
XX	AC AAD03030;
DT	31-MAY-2001 (first entry)
XX	Flax legumin-like seed storage protein DNA.
DE	Flax; seed-specific promoter; legume-like storage protein; seed oil;
XX	protein expression; anticoagulant; cytokine; growth factor; pectinase;
KW	interleukin; alpha-1-antitrypsin; anti-obesity protein; haemoglobin;
KW	serum albumin; insulin; lactoferrin; myoglobin; pulmonary surfactant;
KW	vaccine; alpha amylase; linin; ds.
OS	Linum usitatissimum.
XX	key Location/Qualifiers
FT	repeat_unit 265..276
FT	repeat_unit /*tag= a
FT	repeat_unit /rpt_type= INVERTED
FT	repeat_unit /note= "Irl inverted repeat"
FT	repeat_unit 281..292
FT	repeat_unit /*tag= b
FT	repeat_unit /rpt_type= INVERTED
FT	repeat_unit /note= "Irl inverted repeat"
FT	repeat_unit 513..524
FT	repeat_unit /*tag= c
FT	repeat_unit /rpt_type= INVERTED
FT	repeat_unit /note= "IR2 inverted repeat"
FT	repeat_unit 535..545

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Db 481 tttgacttcgatttcagtttaggtgttgaaatttttcaggttcocattgtgaagccttt 540
Qy 541 tgcattcttgagttattgaaatcgaggtgacatttttttttcaacgtgtccaatcaatcca 600
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Qy 1501 aataatgaaccccttagactttatatttgaattaaaaataaatttaacttttag 1560
Db 1501 aataatgaaccccttagactttatatttgaattaaaaataaatttaacttttag 1560

RESULT 2

AAD03028
ID AAD03028 standard; DNA; 3501 BP.
XX
AC AAD03028;
XX
DT 31-MAY-2001 (first entry)
XX
DE Flax 18.6 kDa oleosin protein DNA.
XX
KW Flax; seed-specific promoter; oleosin protein; seed oil; vaccine;
KW protein expression; anticoagulant; cytokine; growth factor; pectinase;
KW interleukin; alpha-I-antitrypsin; anti-obesity protein; haemoglobin;
KW serum albumin; insulin; lactoferrin; myoglobin; pulmonary surfactant;
KW alpha amylase; ds.
XX
OS Linum usitatissimum.
XX
FH Key Location/Qualifiers
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FT FT /*tag= a
FT FT /rpt_type= DIRECT
FT FT /note= "R1 direct repeat"
FT repeat_unit 80..89
FT FT /*tag= b
FT FT /rpt_type= DIRECT
FT FT /note= "R2 direct repeat"
FT repeat_unit 177..186
FT FT /*tag= c
FT FT /rpt_type= DIRECT
FT FT /note= "R3 direct repeat"
FT repeat_unit 837..846
FT FT /*tag= d
FT FT /rpt_type= DIRECT
FT FT /note= "R3 direct repeat"
FT repeat_unit 1281..1290
FT FT /*tag= e
FT FT /rpt_type= DIRECT

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FT	repeat_unit	/note= "R2 direct repeat"
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FT		1477..1486
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FT		/rpt_type= DIRECT
FT	repeat_unit	/note= "R4 direct repeat"
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FT		/*tag= i
FT		/rpt_type= DIRECT
FT	repeat_unit	/note= "R5 direct repeat"
FT		1678..1687
FT		/*tag= j
FT		/rpt_type= DIRECT
FT	CDS	/note= "R5 direct repeat"
FT		1853..2395
FT		/*tag= k
FT		/product= "Flax 18.6kDa o
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PN	WO200116340-A1.	

WO200116340-A1.

08-MAR-2001.

25-AUG-2000: 2000WO-CA00988.

27-AUG-1999: 99US-0151044

27-OCT-1999; 99US-0161722.
20-MAY-2000; 2000CA-2370304

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(CSIR) COMMONWEALTH SCI & IND

Chaudhary S, Van Rooijen G, Moloney M

WPT: 2001-226693/23.

P-PSDB; AAY72900.

Expressing non-na

comprises using seed-specific promoters obtained from flax -
Claim 14; Fig 2; 68pp; English.

The present sequence is a DNA e

The present invention relates to a method for expressing non-native genes in flax seeds. The method comprises introducing a chimeric nucleic acid construct containing a seed-specific promoter obtained from flax and a nucleic acid which is non-native to the promoter, into a flax plant cell and growing the plant cell into a mature flax plant capable of setting seed, where the nucleic acid is expressed in the seed under the control of the promoter. The seed-specific promoters obtained from flax are useful for modifying the protein, oil or polysaccharide composition of the flax seeds and seeds of other plant species. The promoters facilitate expression of proteins, including sulphur-rich protein that are found in lupins or Brazil nuts in a seed deficient in sulphurous amino acids, peptides having pharmaceutical value such as anticoagulants, antibodies, vaccines, cytokines, growth factors, interleukins, mammalian proteins, including alpha-1-antitrypsin, anti-obesity proteins, haemoglobin, blood proteins, human serum albumin, insulin, lactoferrin, myoglobin, pulmonary surfactants and proteins of industrial value such as alpha-amylase, arabinase, amylglucosidase, catalase, cellobiohydrolase, pectinases, phytase, papain and xylanase.

Sequence 3501 BP; 1007 A; 777 C; 781 G; 936 T; 0 other;

Query Match

3.0%: score 61; DB 22; Length 3501:

[illegible]

PN WO200200928-A2.
XX 03-JAN-2002.
XX 02-JUL-2001; 2001WO-EP07537.
XX 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
XX Claim 1; SEQ ID NO 2046; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
XX Sequence 40862 BP; 14301 A; 414 C; 7426 G; 18721 T; 0 other;
SQ

Query Match 2.5%; Score 51; DB 24; Length 40862;
Best Local Similarity 46.7%; Pred. NO. 0.027;
Matches 194; Conservative 0; Mismatches 220; Indels 1; Gaps 1;
QY 1380 attgatacttactcttgccttcaaaattcttggcagaaacaaattcattagattagaa 1439
Db 21644 ATTAAATTATTTATATATATCCCTATTAAATATCCAAATAATAACATTTTATTATAA 21595
QY 1440 ctggaacacagagtgatgagcggatlaagtcagatcccaacagaggtacatctcttaag 1499
Db 21584 TTTTATTTACTATATAAAATAAATAATTAATAATTTCTTAAATACAAATATTAAATAT 21525
QY 1500 aaataatgtaaccccttgagcttctatatatttgcatttaaaaaataatttaactttta 1559
Db 21524 ATTTAAACCATATTTTTCATTCTACATATTATATAATAAAAAATAAAATAAA-TTAA 21466
QY 1560 gactttatatagtttttaataactaagtttaaccactctatttttatatogaaactat 1619
Db 21465 TCTTTTAAAAATATATAATATACTAATTTTAAATTTATCAATAAAAAATAATTTAAAAAT 21406
QY 1620 ttgatgtctccctcgaataaacttggtattgtgtttacagaacctataatcaataaa 1679
Db 21405 ATTAAATCTTTAAATACAAAAATATTTAAATAATACITAAACATTTAAACCTTAATA 21346
QY 1680 tcaataactcaagaggtttgtcaggttaattgaaggattaacggccaatgcaactag 1739
Db 21345 TACCACATTTCTTTAAATTCATACATCTTAAACCTTAAATTTCAATAAAAAATAAACCAT 21286
QY 1740 tattatcaacgaatagattccactagatgcccatttccatcaatcatcgcgc 1794
Db 21285 TCATAATATCTCCCTTAACAAAAAANTTACTAANTACATTTTCAAAAAACCTTAATACC 21231

RESULT 6
AAZ37082
ID AAZ37082 standard; DNA; 1431 BP.
XX
AC AAZ37082;
XX
DT 27-MAR-2000 (first entry)

XX DNA sequence encoding a yeast SceI endonuclease.
DE
XX
XX SceI endonuclease; phosphodiester bond; yeast; genetic engineering;
KW PCR; polymerase chain reaction; gene cloning; ss.
XX
XX Saccharomyces cerevisiae.
XX
XX Key Location/Qualifiers
FH 1..1431
FT /tag= a
FT /product= "SceI endonuclease"
FT /note= "contains 5 stop codons"
XX
XX EP972836-A2.
XX 19-JAN-2000.
XX 21-MAY-1999; 99EP-0110008.
XX 22-MAY-1998; 98JP-0141861.
XX (RIKA) INST PHYSICAL & CHEM RES.
XX Morishima N, Shibata T, Mizumura H;
PI
XX WPI; 2000-099856/09.
XX P-PSDB; AAV54040.
XX New modified endonuclease capable of recognizing specific nucleotide
PT sequence, useful for genetic engineering techniques -
PT
XX Disclosure; Fig 4; 43pp; English.
XX
XX The present sequence encodes a yeast SceI endonuclease. The
CC endonuclease hydrolyses the phosphodiester bond of a polynucleotide
CC chain. The endonuclease is the 50 kDa subunit of a yeast endonuclease.
CC The endonuclease gene was modified so that it could be
CC mass-produced in an expression system such as E. coli or yeast. The
CC endonuclease polynucleotide sequence was modified by substituting
CC codons that are unique to mitochondria (the gene is expressed in
CC mitochondria) with universal codons. The endonuclease cuts molecules
CC within sequence AA37078, and is therefore useful in genetic engineering
CC techniques such as PCR (polymerase chain reaction) for cloning,
CC amplifying and analysing genes.
XX
XX Sequence 1431 BP; 647 A; 87 C; 103 G; 594 T; 0 other;
SQ

Query Match 2.4%; Score 48.6; DB 21; Length 1431;
Best Local Similarity 54.9%; Pred. NO. 0.026;
Matches 96; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1515 tttagactttatatatttgcaattaaaaataatttaacttttagactttatatagtt 1574
Db 1223 tttaacctttacatgataataacaaatttaattataattaaatttagatttaacttatta 1282
QY 1575 tttaataactaagtttaaccactctattttatattatcgaactattttgtatgctccct 1634
Db 1283 ttaaatcataattgaaataatagagattttgttttagttattctgaataatacaata 1342
QY 1635 ctataataaacttgattgttttcagaaacctataatcaataatcaatactca 1689
Db 1343 atataataattgataattgatattattattataataataataataataca 1397

RESULT 7
AAQ24134
ID AAQ24134 standard; DNA; 1671 BP.
XX
AC AAQ24134;
XX
DT 09-NOV-1992 (first entry)

```

XX DE 50 kD subunit of SceI.
XX
XX Endonuclease SceI; PAGE; chromatography; ENS2 gene; ss.
KW
XX Sacchromyces cerevisae.
XX
XX Key Location/Qualifiers
FH CDS 1..1589 /tag= a
FT /label= SceI_50kD_subunit
FT 1..81
FT /tag= b
FT /number= 1
FT intron 82..158 /tag= c
FT /number= 1
FT exon 159..1586 /tag= d
FT /number= 2
XX
XX JP04104793-A.
XX
XX 07-APR-1992.
XX
XX 21-AUG-1990; 90JP-0219566.
XX
XX 21-AUG-1990; 90JP-0219566.
XX
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX
XX WPI; 1992-164281/20.
XX
XX P-PSDB; AAR22667.
XX
XX ENS2 gene encoding 50kD subunit of SceI endonuclease - used for mass
XX prodn. of recombinant endonuclease in eg. Sacchromyces IAM4274
XX
XX Claim 1; Page 2; 4pp; Japanese.
XX
XX The sequence given encodes the 50kD subunit of endonuclease SceI.
CC Endonuclease SceI can be mass produced from the 50kD subunits
CC expressed from the ENS2 gene. The 50kD subunit was purified by
CC treating SceI from eg. Sacchromyces IAM4274, and by denaturing the
CC protein and subjecting it to PAGE, or by chromatography on a
CC phosphocellulose column.
XX
XX Sequence 1671 BP; 769 A; 108 C; 113 G; 681 T; 0 other;
SQ
Query Match 2.4%; Score 48.6; DB 13; Length 1671;
Best Local Similarity 54.9%; Pred. No. 0.028;
Matches 96; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1515 tttagacttatatttgcaattaaataaaataatttaacttttagactttatatagt 1574
DB 1381 tttagacttatatttgcaattaaataaaataatttaacttttagactttatatagt 1440
QY 1575 tttaataactaaagttaaaccactctattttatatcgaaactattttagtctccct 1634
DB 1441 ttaatacatataattgaaataaataagagatttggtttagtattctgaatatcaata 1500
QY 1635 ctaataaacttggtattgtgtttacagaacacctataatacaataaactcaactca 1689
DB 1501 atattaaattgataattgattattattattattattattattattattattattata 1555
RESULT 8
ABL33732/c
ID ABL33732 standard; DNA; 5883 BP.
XX
XX ABL33732;
XX
XX 26-MAR-2002 (first entry)
DT

```

```

XX Human immune system associated gene SEQ ID NO: 1705.
DE
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytosatic; neutropenic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmologic;
KW antirheumatic; antiarthritis; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX WO200200928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07537.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX
XX 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
XX for diagnosis and treatment of diseases associated with abnormal
XX cytosine methylation
XX
XX Claim 1; SEQ ID NO 1705; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.
XX
XX Sequence 5883 BP; 1526 A; 80 C; 1224 G; 3053 T; 0 other;
SQ
Query Match 2.4%; Score 48.2; DB 24; Length 5883;
Best Local Similarity 49.3%; Pred. No. 0.06;
Matches 180; Conservative 0; Mismatches 183; Indels 2; Gaps 2;
QY 1422 caattcattagattagaactggaaaccagagtgatgagcggattaaagtgcagattccaac 1481
DB 1257 CCATTTAATAATAAATTTTAAATAAATAAATAATCATACTTATATTTATATAAAT 1198
QY 1482 agagttaacattcttaagaataatgttaacccttttagactttatatattlgecaataaa 1541
DB 1197 AATTAAATATTATATAAACAATTATAACAATCAATTTAAATTAACCTTAAACTAAATAA 1138
QY 1542 aaaaataatttaacttttagact-ttatatatagttttaaataacttaagcttaaccactcta 1600
DB 1137 TAAATAATAAATTTTATATAATCTTAATTAATAATATATATATACATAAATCAATCTTAAC 1078
QY 1601 ttatttatcgaaac-tattttagtctctccctctaaataaacttggtattgttta 1659
DB 1077 TAAATAACTTCAATACATAATAATCTTTTCTTTTAAATAAATAATCTTACTCTATTA 1018
QY 1660 cagaacctataatacaataataactcaactgaactgaatttgcagtttaataaaggat 1719
DB 1017 CCCAAACTAAATAACATAATAAATCTCAACCAACTCTACCTCTCTAAATCAACAAT 958
QY 1720 taacggccaaatgcactagtagtattatcaacgaatagattcacactagatggcattcc 1779

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ov 1607 atatcgaaactatttctgtatgtctccctctaaataaaacttggatattgtgtttacagaacc 1666

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 13:11:16 ; Search time 133.71 Seconds
(without alignments)
9183.471 Million cell updates/sec

Title: US-09-645-593-8

Perfect score: 4999

Sequence: 1 ctcaagatacagacaagg.....tcnattgtanattgncgttg 4999

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129.6	2.6	3113	1	US-08-146-422-20
2	129.6	2.6	3113	1	US-08-626-554-2
3	102.4	2.0	1685	1	US-08-486-721A-1
4	101.2	2.0	1556	1	US-08-486-721A-2
5	68.8	1.4	7218	1	US-08-232-463-14
6	61.2	1.2	7218	1	US-08-232-463-14
7	47.4	0.9	1240	1	US-08-142-393-2
8	45.4	0.9	1431	4	US-09-316-083-2
9	43.8	0.9	8920	2	US-08-446-855A-1
10	43.8	0.9	8920	4	US-09-150-741-1
11	43.4	0.9	5923	4	US-09-064-922-3
12	42.4	0.8	3319	2	US-08-960-022-19
13	42.2	0.8	663	4	US-08-998-416-191
14	42	0.8	854	4	US-08-998-416-534
15	41.6	0.8	68750	3	US-09-335-409-1
16	41.6	0.8	68750	4	US-09-568-102-1
17	41.6	0.8	68750	4	US-09-567-969-1
18	41.6	0.8	68750	4	US-09-568-480-1
19	41.6	0.8	68750	4	US-09-568-486-1
20	41.6	0.8	68750	4	US-09-568-472-1
21	41.4	0.8	662	4	US-08-998-416-185
22	41.4	0.8	665	4	US-08-998-416-937
23	41.4	0.8	701	4	US-08-998-416-701
24	41.4	0.8	711	4	US-08-998-416-786
25	41.4	0.8	724	4	US-08-998-416-683
26	41.4	0.8	732	4	US-08-998-416-1036
27	41.4	0.8	828	4	US-08-998-416-538

C 28	41.4	0.8	834	4	US-08-998-416-305	Sequence 305, Appl
29	41.4	0.8	860	4	US-08-998-416-287	Sequence 287, Appl
30	40.4	0.8	289	4	US-09-007-005-17	Sequence 17, Appl
31	40.4	0.8	289	4	US-09-244-796-17	Sequence 17, Appl
32	40.4	0.8	636	4	US-08-998-416-1137	Sequence 1137, Appl
33	40.4	0.8	837	4	US-08-998-416-288	Sequence 288, Appl
C 34	40.2	0.8	5495	1	US-08-602-010A-1	Sequence 1, Appl
35	40.2	0.8	5495	1	US-08-602-010A-2	Sequence 2, Appl
C 36	40.2	0.8	5495	1	US-08-680-726A-1	Sequence 1, Appl
37	40.2	0.8	5495	1	US-08-680-726A-2	Sequence 2, Appl
C 38	40.2	0.8	5495	3	US-09-092-409-1	Sequence 1, Appl
39	40.2	0.8	5495	3	US-09-092-409-2	Sequence 2, Appl
C 40	40.2	0.8	10592	1	US-08-680-726A-51	Sequence 51, Appl
41	40.2	0.8	10592	1	US-08-680-726A-52	Sequence 52, Appl
C 42	40.2	0.8	10592	1	US-09-092-409-51	Sequence 51, Appl
43	40.2	0.8	10592	3	US-09-092-409-52	Sequence 52, Appl
C 44	39.6	0.8	1125	4	US-09-516-914-12	Sequence 12, Appl
C 45	39.6	0.8	1298	1	US-08-473-157A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-146-422-20
; Sequence 20 Application US/08146422
; Patent No. 5543576
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; APPLICANT: QUAX, WILHEMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146.422
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/POCKET NUMBER: 44615-20011.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-146-422-20

Query Match 2.6%; Score 129.6; DB 1; Length 3113;
Best Local Similarity 55.0%; Pred. No. 2.8e-27;

Matches 275; Conservative 0; Mismatches 224; Indels 1; Gaps 1;

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QY 3325 tatctgaccgacgggtttgaatttttaggaagcgatcagggtgcgcgaactggaacatca 3384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2437 TCTCAGCCCTCCCTGGATCTATCCGTCAAAACCGATGGTGTCTCCACAGTGGAAACGCAA 2496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3385 acgcacacagcatagtgatcgatcagagcaacagcagatccagatcgtgaacgag 3444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2497 ACGCAACCGCGTCTCTACGTACAGACGGGGAACCCATGTGCAGGTGGTTAACGACA 2556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3445 aagggaattcgtgttcgatggagtgctgcaggaagacaggtggtgacggtgcgcgaga 3504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2557 ACGGTGACAGAGTCTCGACGACAAAGTCTCTCAAGGACAGGTACTTCCATACCAACAA 2616
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3505 attcgcgggtggaagatccagacgagaggttttagtggtggtgcgttcaagacca 3564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2617 GTTTCCTCGTGGTGAACCGGCAACAGCAAGCAAGTTCGGTGGATCGAGTTCAAGACAA 2676
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QY 3565 acgacaacgcatggtgaaactcgttagcggggagggacatcggtgaaggcgatccccc 3624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2677 ACGCAACCGCACAGATCAACACACTTCTGTCGACGAACCTCGGTCTTTAGAGGTTTACCAT 2736
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3625 cggatgtactggctaaacgctgaggtgtcgcgagagagcgagaggtgaaagtcca 3684
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Db 2737 TAGAGGTTCATCCATGGTGTACCAATCTCACTCGNAGAGCAAGAAGGTTAAGTTCA 2796
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QY 3685 acaggcaggagactcaactcgttagcaccagggggcagtcagggtcgcggggaggttga 3744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2797 ACACGATCGAGACCACTTTACGCACACAGCAGTGGCCGAGTAGCTACGGAGGGCCAAAGGA 2856
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QY 3745 atgctgcagagaggtgataactcgtttagttaaattgacggtgaaataataacggt 3804
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2857 AGGCTGATGCTTAGAGCTTACCAGTACCACTCTACTGTATAAAG-CAAGTTAAATAGTA 2915
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 2

```

US-08-626-554-2
; Sequence 2, Application US/08626554
; Patent No. 5714474
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRILJ
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; APPLICANT: QUAX, WILHEMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,554
; FILING DATE: 02-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959

```

```

; REFERENCE/DOCKET NUMBER: 26192-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-626-554-2

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Query Match 2.6%; Score 129.6; DB 1; Length 3113;
Best Local Similarity 55.0%; Pred. No. 2.8e-27;
Matches 275; Conservative 0; Mismatches 224; Indels 1; Gaps 1;

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QY 3325 tatctgaccgacgggtttgaatttttaggaagcgatcagggtgcgcgaactggaacatca 3384
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Db 2437 TCTCAGCCCTCCCTGGATCTATCCGTCAAAACCGATGGTGTCTCCACAGTGGAAACGCAA 2496
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QY 3385 acgcacacagcatagtgatcgatcagagcaacagcagatccagatcgtgaacgag 3444
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Db 2497 ACGCAACCGCGTCTCTACGTACAGACGGGGAACCCATGTGCAGGTGGTTAACGACA 2556
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QY 3445 aagggaattcgtgttcgatggagtgctgcaggaagacaggtggtgacggtgcgcgaga 3504
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QY 3505 attcgcgggtggaagatccagacgagaggttttagtggtggtgcgttcaagacca 3564
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QY 3685 acgacaacgcatggtgaaactcgttagcggggagggacatcgagggtgcggggaggttga 3744
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Db 2797 ACACGATCGAGACCACTTTACGCACACAGCAGTGGCCGAGTAGCTACGGAGGGCCAAAGGA 2856
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QY 3745 atgctgcagagaggtgataactcgtttagttaaattgacggtgaaataataacggt 3804
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Db 2857 AGGCTGATGCTTAGAGCTTACCAGTACCACTCTACTGTATAAAG-CAAGTTAAATAGTA 2915
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3805 aaatatatgtaataataat 3824
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2916 ATAAAAAGAGTAATAATAAT 2935
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 3

```

US-08-486-721A-1
; Sequence 1, Application US/08486721A
; Patent No. 5739025
; GENERAL INFORMATION:
; APPLICANT: Fukazawa, Chikafusa
; TITLE OF INVENTION: Method of Producing
; TITLE OF INVENTION: Asparaginyl Endoprotease
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frishauf, Holtz, Goodman, Langer & Chick
; STREET: 767 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017-2023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3+ inch, 1.4 mb

```

```
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,721A
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/091,991
FILING DATE: 12-JULY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard S.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 930587/HG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 319-4900
TELEFAX: (212) 319-5101
TELEX: 236268
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: c-DNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Oat (Avena sativa, L.)
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: middle stage
HAPLOTYPE: 2n
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE: cotyledon
IMMEDIATE SOURCE:
CLONE: A2B
LIBRARY: cDNA library
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: Oat 12S globulin / 11-S protein Family
LOCATION: protein bodies of cotyledonary tissue
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
US-08-486-721A-1

Query Match 2.0%; Score 102.4; DB 1; Length 1685;
Best Local Similarity 56.2%; Pred. No. 1.6e-19;
Matches 190; Conservative 1; Mismatches 147; Indels 0; Gaps 0;

Qy 3352 aggaagcagatcaggtgcccgaactggaacatcaacacacagcatagtgatcgagatca 3411
Db 1140 AGAATGCTATTCTTTCACCATCTGGATCATCAATGCACACAGTGTGGTCTACATGATCC 1199
Qy 3412 gaggaacagcagagtcagatcgtagaacgaggaattcggtgttcgatggagtc 3471
Db 1200 AAGGCATGCTCAAGTTCAGATTGCTCAATAACAATGCTCAGACTGTATTCAATGACCGTC 1259
Qy 3472 tgcaggaaggacaggtggtgacggtgccgcagaaacttcggtggttaagagatccaga 3531
Db 1260 TTCGCCAGGTCACTTGTGTTATCTGTAACCAACACTACGTGTTCTCAAGGCGCGGAGC 1319

COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,721A
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/091,991
FILING DATE: 12-JULY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard S.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 930587/HG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 319-4900
TELEFAX: (212) 319-5101
TELEX: 236268
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: c-DNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Oat (Avena sativa, L.)
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: middle stage
HAPLOTYPE: 2n
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE: cotyledon
IMMEDIATE SOURCE:
CLONE: A2B
LIBRARY: cDNA library
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: Oat 12S globulin / 11-S protein Family
LOCATION: protein bodies of cotyledonary tissue
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
US-08-486-721A-1

Qy 3532 qcagagagtttgagtggtggttcacacacacacacagcgatggtgaactcgctag 3591
Db 1320 GTGAAGGATGCCAGTATATCTCATTAAGACCAACCAACTCCATCGTTAGCCACATCG 1379
Qy 3592 ccgagagagcatcgagtcagtgagcgatcccccgcgagtgatgctactggctaacgcctggaggg 3651
Db 1380 CTGGAAGAGCTCCATTCTTCTCGTTCCTTGCTGGATGCTCTGCCCAATGTCATACCGCA 1439
Qy 3652 tgcgcgcgagagagcgagagagaggtgaagtcaacagg 3689
Db 1440 TTTCAGGCAAGAGCCGCCGAAACCTCAAAAAACACAGG 1477

RESULT 4
US-08-486-721A-2
Sequence 2, Application US/08486721A
Patent No. 5739025
GENERAL INFORMATION:
APPLICANT: Fukazawa, Chikafusa
TITLE OF INVENTION: Method of Producing
TITLE OF INVENTION: Asparaginyl Endoprotease
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frischauf, Holtz, Goodman, Langer & Chick
STREET: 767 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017-2023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3+ inch, 1.4 mb
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,721A
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/091,991
FILING DATE: 12-JULY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard S.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 930587/HG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 319-4900
TELEFAX: (212) 319-5101
TELEX: 236268
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: c-DNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Oat (Avena sativa, L.)
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: middle stage
HAPLOTYPE: 2n
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE: cotyledon
IMMEDIATE SOURCE:
LIBRARY: cDNA library
CLONE: A1B
POSITION IN GENOME:
```

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; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: Oat 12S globulin / 11-S protein family
; LOCATION: protein bodies of cotyledonary tissue
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; US-08-486-721A-2

Query Match          2.0%; Score 101.2; DB 1; Length 1556;
Best Local Similarity 56.2%; Pred No. 3.5e-19;
Matches 190; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 3352 aggaagcatcaggtggtgacgacatcaacacagcagcatagtgtacgcgata 3411
  || || || || || || || || || || || || || || || || || || ||
Db 1011 AGAATGCTATTTTCCACCATTCGGAACATCAATGCACATAGTGTGCTACATGATTC 1070

QY 3412 gagacaacagatccagatcgtaacgaggaaggaattcggtgttcgatgagtc 3471
  || || || || || || || || || || || || || || || || || || ||
Db 1071 AAGGGATGCTCGAGTTCAAGTTGTCAATAAACAATGTCAGACTGTATTCAATGACCGTTC 1130

QY 3472 tcgagaagagacaggtggtgacggtgcccagaaacttcggtggttaagagatccca 3531
  || || || || || || || || || || || || || || || || || || ||
Db 1131 TTCCCAAGGTGCTAGTTGCTTAATCTTACCACACACTACCTGTTCTCAAGAAGACGGAGC 1190

QY 3532 qcagagaggttgaagtggtggttcgaagcaacacagcagcatggtgaactcgta 3591
  || || || || || || || || || || || || || || || || || || ||
Db 1191 GTGAAGATGCCAGTATATCTCATTCAGACCAACCAACCTCAATGTTAGCCATG 1250

QY 3592 ccggagagacatcgagtaagggcgtaccccgcgatgactggtacgcctgaggg 3651
  || || || || || || || || || || || || || || || || || || ||
Db 1251 CTGGAAGAGCTCCATCTTCGTGCTGCTGCGGTGAATGCTCGCAATGCATACCGCA 1310

QY 3652 tgcgcggagagggcgagggaggggtgaagtcaacagg 3689
  || || || || || || || || || || || || || || || || || || ||
Db 1311 TTCCAGGCAAGAGTCCGAACCTCAAAACCAACAGG 1348

RESULT 5
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
```

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; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fis
; US-08-232-463-14

Query Match          1.4%; Score 68.8; DB 1; Length 7218;
Best Local Similarity 7.6%; Pred No. 3.5e-09;
Matches 34; Conservative 235; Mismatches 177; Indels 0; Gaps 0;

QY 3440 cgaggaaggaattcggtgttcgatgagtgctgcaggaagacacagtggtgacggtgcc 3499
  || || || || || || || || || || || || || || || || || || ||
Db 1508 CAAAAACGGCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAGAGATA 1449

QY 3500 gcagaaacttcggtggttaagagatccagagcgagaggtttgagtggtggtlcaa 3559
  || || || || || || || || || || || || || || || || || || ||
Db 1448 GAAGAAATTGCTACACACACACACACACACACACACACACACACACACACACACAC 1389

QY 3560 gaccacacacacacacacacacacacacacacacacacacacacacacacacacacac 3619
  || || || || || || || || || || || || || || || || || || ||
Db 1388 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1329

QY 3620 cccgcgcatgtactgctaacgctgaggtgtcgcgagagagcgagagaggggaa 3679
  || || || || || || || || || || || || || || || || || || ||
Db 1328 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1269

QY 3680 gtlcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3739
  || || || || || || || || || || || || || || || || || || ||
Db 1268 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1209

QY 3740 gttgaatgctlcaagagaggtgatcaactgtctatgtataaatgtgacggtgaaataa 3799
  || || || || || || || || || || || || || || || || || || ||
Db 1208 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1149

QY 3800 acggttaataatataataataataataataataataataataataataataataataata 3859
  || || || || || || || || || || || || || || || || || || ||
Db 1148 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1089

QY 3860 ggaatgtgtaagcagcagtagccg 3885
  || || || || || || || || || || || || || || || || || || ||
Db 1088 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1063

RESULT 6
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
```


APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1076UP
US-08-998-416-191

Query Match 0.8%; Score 42.2; DB 4; Length 663;
Best Local Similarity 49.4%; Pred. No. 0.037;
Matches 132; Conservative 2; Mismatches 130; Indels 3; Gaps 1;
QY 1380 attgataaattactcttcttgcataattcttggcagaaacaaattcattagattagaa 1439
DB 219 ATTATTAGATTAAAGTATCTTAAATAATATATTATTAGGTAATAATATTAGTAGGTAGTAA 278
QY 1440 ctggaaccagagtgatgagcggattgaagtcagattcccaacagagttacatctcttaag 1499
DB 279 TATCCAAATTARRGGGTAGACTATTAAATAGAAATATTACTAGACTAAATAAATAATAT 338
QY 1500 aaataatgaacccctttagactttatatatttgcataataaaataaatttaacttta 1559
DB 339 TATGAAGGTACATTAAATAATTATATATATATATATATATATATATATATATATATATAT 395
QY 1560 gactttatatagttttaataaactgaagtttaaccactctattatttatatcgaaactat 1619
DB 396 TAAATTAATTAAT 455
QY 1620 ttgtatgtctccctctctaaataaacttggtattgtgtttacagaaacctataatcaaat 1677
DB 456 TGGTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 482

RESULT 14
US-08-998-416-534

Sequence 534, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 534:
SEQUENCE CHARACTERISTICS:
LENGTH: 854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1372UP
US-08-998-416-534

Query Match 0.8%; Score 42; DB 4; Length 854;
Best Local Similarity 48.7%; Pred. No. 0.051;
Matches 145; Conservative 0; Mismatches 150; Indels 3; Gaps 1;
QY 1380 attgataaattactcttcttgcataattcttggcagaaacaaattcattagattagaa 1439
DB 219 ATTATTAGATTAAAGTATCTTAAATAATATATTATTAGGTAATAATATTAGTAGGTAGTAA 278
QY 1440 ctggaaccagagtgatgagcggattgaagtcagattcccaacagagttacatctcttaag 1499
DB 279 TATCCAAATTAAAGGTAGACTATTAAATAATATATATATATATATATATATATATATATAT 338
QY 1500 aaataatgaacccctttagactttatatatttgcataataaaataaatttaacttta 1559
DB 339 TATGAAGGTACATTAAATAATTATATATATATATATATATATATATATATATATATATAT 395
QY 1560 gactttatatagttttaataaactgaagtttaaccactctattatttatatcgaaactat 1619
DB 396 TAAATTAATTAAT 455
QY 1620 ttgtatgtctccctctctaaataaacttggtattgtgtttacagaaacctataatcaaat 1677

